Listing of the Claims:

1-25 (Canceled)

26. (Previously Amended) A method of screening for genetic markers in a sample of polynucleotides, comprising:

(a) providing a sample of polynucleotides;

(b) hybridizing said sample to a set of at least 100 beads, each of which comprise a different probe nucleic acid that is between 25 and 100 nucleotides in length, said beads being coded with an encoding system whereby the target specific sequence of each probe nucleic acid attached to the beads can be identified; and

(c) detecting hybridization of said sample polynucleotides to said beads, thereby screening for genetic markers in the sample.

27.(Previously Presented) A method of claim 26, wherein the method screens for tens of different genetic markers.

28.(Previously Presented) A method of claim 26, wherein the method screens for hundreds of different genetic markers.

29. (Previously Presented) A method of claim 26, wherein the method screens for thousands of different genetic markers.

30.(Previously Presented) A method of claim 26, wherein the method generates correlations useful for the detection of a causative mutation leading to a medical condition.

31.(Canceled)

32.(Previously Presented) A method of claim 26, wherein the probe nucleic acids are greater than fifty nucleotides in length.

33.(Previously Presented) A method of claim 32, wherein the probe nucleic acids are 50 nucleotides in length.

34.(Previously Presented) A method of claim 26, wherein the presence or absence of a particular genetic marker sequence is determined.

35.(Previously Presented) A method of claim 26, wherein said sample of polynucleotides is a pool of DNA or RNA.

36.(Previously Presented) A method of claim 26, wherein said sample of polynucleotides is amplified from a biological sample by an *in vivo* or *in vitro* method.

37.(Previously Presented) A method of claim 26, wherein said sample polynucleotides comprise fluorescently labeled nucleic acids.

38.(Previously Presented) A method of claim 26, wherein said probe nucleic acids are oligonucleotides.

39.(Previously Presented) A method of claim 26, wherein the encoding system is selected from the group consisting of a magnetic system, a shape encoding system, a color encoding system, and combinations thereof.

40.(Previously Presented) A method of claim 26, wherein the detecting comprises the detection of the signal from at least one fluorescent label.

41.(Previously Presented) A method of claim 40, wherein the signal from the fluorescent label associated with each bead is transferred directly to the detector.

42.(Previously Presented) A method of claim 26, wherein the probes nucleic acids hybridize to gene alleles correlated with specific genetic deficiencies.

43.(Previously Presented) A method of claim 26, wherein the hybridizing discriminates between perfect matching and imperfect matching between the probe and sample polynucleotides.

44.(Previously Presented) A method of claim 26, further comprising:

(d) analyzing data from the hybridization to correlate particular genetic markers with the sample.

45.(Previously Presented) A method of claim 44, wherein the sample is from a patient with a medical condition.

46.(Previously Amended) A method of correlating a medical condition with genetic markers in a polynucleotide sample, comprising:

(a) providing at least one sample of polynucleotides;

(b) hybridizing said sample to a set of at least 100 beads, each of which comprise a different probe nucleic acid attached thereto that is between 25 and 100 nucleotides in length, said beads being coded with an encoding system whereby the target specific sequence of each probe nucleic acid attached to the beads can be identified; and;

(c) detecting hybridization of said sample polynucleotides to said beads to produce hybridization data; and

(d) analyzing the hybridization data to correlate the medical condition with particular genetic markers.

47.(Previously Presented) A method of claim 46, wherein the method is applied to a large population to allow statistical analysis.

48.(Previously Presented) A method of claim 46, wherein the method screens for tens of different genetic markers.

49.(Previously Presented) A method of claim 46, wherein the method screens for hundreds of different genetic markers.

50. (Previously Presented) A method of claim 46, wherein the method screens for thousands of different genetic markers.

51.(Previously Presented) A method of claim 46, wherein said sample of polynucleotides is amplified from a biological sample by an *in vivo* or *in vitro* method.

52.(Previously Presented) A method of claim 46, wherein said sample polynucleotides comprise fluorescently labeled nucleic acids.

53.(Previously Presented) A method of claim 46, wherein said probe nucleic acids are oligonucleotides.

54.(Previously Presented) A method of claim 46, wherein the encoding system is selected from the group consisting of a magnetic system, a shape encoding system, a color encoding system, and combinations thereof.

55.(Previously Presented) A method of claim 46, wherein the detecting comprises the detection of the signal from at least one fluorescent label.